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# 2

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,607

DATE: 04/23/2001

TIME: 13:23:01

Input Set : A:\Stk070.app

Output Set: N:\CRF3\04232001\I828607.raw

3 <110> APPLICANT: STRYKER CORPORATION  
 5 <120> TITLE OF INVENTION: REPAIR OF LARYNX, TRACHEA, AND OTHER FIBROCARILAGINOUS  
 6 TISSUES  
 8 <130> FILE REFERENCE: STK-070 PCT  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/828,607  
 C--> 11 <141> CURRENT FILING DATE: 2001-04-06  
 13 <160> NUMBER OF SEQ ID NOS: 9  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1822  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: CDS  
 24 <222> LOCATION: (49)..(1341)  
 26 <400> SEQUENCE: 1  
 27 ggtgctggggcc cggagcccgagg agcccgggta ggcgcgtagag ccggcgcg atg cac gtg 57  
 28 Met His Val  
 29 1  
 31 cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105  
 32 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala  
 33 5 10 15  
 35 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153  
 36 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn  
 37 20 25 30 35  
 39 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201  
 40 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg  
 41 40 45 50  
 43 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249  
 44 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg  
 45 55 60 65  
 47 ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297  
 48 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met  
 49 70 75 80  
 51 ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc gcc 345  
 52 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly  
 53 85 90 95  
 55 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393  
 56 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly  
 57 100 105 110 115  
 59 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441  
 60 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp  
 61 120 125 130  
 63 atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc 489  
 64 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe  
 65 135 140 145  
 67 cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc 537

ENTERED

See p.5

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68 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
69      150      155      160
71 cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac 585
72 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
73      165      170      175
75 tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat 633
76 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
77 180      185      190      195
79 cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc 681
80 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
81      200      205      210
83 gac agc cgt acc ctc tgg gcc tcg gag gag gcc tgg ctg gtg ttt gac 729
84 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
85      215      220      225
87 atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg 777
88 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
89      230      235      240
91 ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc 825
92 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
93      245      250      255
95 aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc 873
96 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
97 260      265      270      275
99 ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc 921
100 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
101      280      285      290
103 cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc 969
104 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
105      295      300      305
107 aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc 1017
108 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
109      310      315      320
111 agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc 1065
112 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
113      325      330      335
115 cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc 1113
116 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
117 340      345      350      355
119 gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg 1161
120 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
121      360      365      370
123 aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac 1209
124 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
125      375      380      385
127 ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc 1257
128 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
129      390      395      400
131 atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305
132 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys

```

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```

133      405      410      415/
135 tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
136 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
137 420      425      430
139 gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411
141 gaaccagcag accaactgcc ttttgtgaga ccttccctc cctatcccca actttaagg 1471
143 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
145 atccaatgaa caagatccta caagctgtgc aggcataacc tagcaggaaa aaaaaacaac 1591
147 gcataaagaa aaatggccgg gccaggtcat tggctgggaa gtctcagcca tgcacggact 1651
149 cgtttccaga ggtaattatg agcgctacc agccaggcca cccagccgtg ggaggaagg 1711
151 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc 1771
153 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaa aaaaaaaaaa a 1822
156 <210> SEQ ID NO: 2
157 <211> LENGTH: 431
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
161 <400> SEQUENCE: 2
162 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
163 1 5 10 15
165 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
166 20 25 30
168 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
169 35 40 45
171 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
172 50 55 60
174 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
175 65 70 75 80
177 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
178 85 90 95
180 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
181 100 105 110
183 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
184 115 120 125
186 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
187 130 135 140
189 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
190 145 150 155 160
192 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
193 165 170 175
195 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
196 180 185 190
198 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
199 195 200 205
201 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
202 210 215 220
204 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
205 225 230 235 240
207 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
208 245 250 255

```

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```

210 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
211           260           265           270
213 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
214           275           280           285
216 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
217           290           295           300
219 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
220 305           310           315           320
222 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
223           325           330           335
225 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
226           340           345           350
228 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
229           355           360           365
231 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
232           370           375           380
234 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
235 385           390           395           400
237 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
238           405           410           415
240 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
241           420           425           430

```

245 &lt;210&gt; SEQ ID NO: 3

246 &lt;211&gt; LENGTH: 102

247 &lt;212&gt; TYPE: PRT

248 &lt;213&gt; ORGANISM: Artificial Sequence

250 &lt;220&gt; FEATURE:

251 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: OPX

253 &lt;220&gt; FEATURE:

254 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one  
 255 or more specified amino acids as defined in the  
 256 specification.

258 &lt;400&gt; SEQUENCE: 3

```

W--> 259 Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
260   1           5           10           15
W--> 262 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
263           20           25           30
W--> 265 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
266           35           40           45
W--> 268 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
269           50           55           60
W--> 271 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
272 65           70           75           80
W--> 274 Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
275           85           90           95
W--> 277 Xaa Ala Cys Gly Cys His
278           100

```

281 &lt;210&gt; SEQ ID NO: 4

282 &lt;211&gt; LENGTH: 97

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Input Set : A:\Stk070.app

Output Set: N:\CRF3\04232001\I828607.raw

283 <212> TYPE: PRT

284 <213> ORGANISM: Artificial Sequence

286 &lt;220&gt; FEATURE:

287 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-7  
289 <220> FEATURE

289 <220> FEATURE:

290 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one  
291 or more specified amino acids.

291 or more specified amino acids as defined in the  
292

292 specification.

294 <400> SEQUENCE: 4

W--> 295 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa  
296 1 5 10 15

W--> 298 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro  
299 20 25 30

W--> 301 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa  
302 35 40 45

W--> 304 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro  
305 50 55 60

W--> 307 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa  
308 65 70 75 80

W--> 310 Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys  
311 85 90 95

W--> 313 Xaa

317 <210> SEQ ID NO: 5

318 <211> LENGTH: 102

319 <212> TYPE: PRT

320 <213> ORGANISM: Artificial Sequence

322 <220> FEATURE:

323 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-8  
325 <220> FEATURE:

325 <220> FEATURE:

326 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one  
327 or more specified amino acids.

327 or more specified amino acids as defined in the

328 specification.

330 <400> SEQUENCE: 5

W--> 331 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa  
332 1 5 10 15

W--> 334 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly  
335 20 25 30

W--> 337 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala  
338 35 40 45

[illegible]

W--> 343 Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa  
344 65 70 75 80

W--> 346 Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val  
347 85 90 95

W--> 349 Xaa Xaa Cys Xaa Cys Xaa  
350 100

353 <210> SEQ ID NO: 6

354 <211> LENGTH: 97

**Please Note:**

**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.**

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,607

DATE: 04/23/2001

TIME: 13:23:02

Input Set : A:\Stk070.app

Output Set: N:\CRF3\04232001\I828607.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:262 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:262 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:271 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:271 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:274 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:274 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:277 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:277 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:295 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:295 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:301 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:301 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:310 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:331 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:331 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:334 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5

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L:334 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:349 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:349 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:367 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:367 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:373 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:373 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:376 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:376 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9